PROCEEDINGS OF TDWG

Biodiversity Information Science and Standards 1: e20394
doi: 10.3897/tdwgproceedings.1.20394

OPEN ACCESS

Conference Abstract

Catalogue of Life, China and Taxonomic Tree Tool

Liqiang Ji ‡

‡ Institute of Zoology, Chinese Academy of Sciences, Beijing, China

Corresponding author: Liqiang Ji (ji@ioz.ac.cn)

Received: 17 Aug 2017 | Published: 17 Aug 2017

Citation: Ji L (2017) Catalogue of Life, China and Taxonomic Tree Tool. Proceedings of TDWG 1: e20394.
https://doi.org/10.3897/tdwgproceedings.1.20394

Abstract

Since 2008, the Species 2000 China Node, with the support of the Chinese Academy of Sciences' Biodiversity Committee, has organized scientists to compile and release the Catalogue of Life, China (CoL China) each year. It follows the Standard Data Set of Species 2000's global Catalogue of Life to collect and release Chinese species data. Considering the local requirement, a Chinese formal name and its Pinyin (a romanized form of the name) are appended in species records. The data items include the accepted scientific name for the species, Chinese name, synonyms, common names, latest taxonomic scrutiny, source database, family, classification above family and highest taxon in the database, distribution, and references. A dynamic distribution map could be shown for each species in the checklist. CoL China 2017 Annual Checklist was released in July 2017 by the Chinese Academy of Sciences and Ministry of Environment Protection in Beijing. The groups of species in the 2017 Annual Checklist and their number of accepted species names include Animalia (38,631), Bacteria (469), Chromista (2,239), Fungi (4,273), Plantae (44,041), Protozoa (1,843) and viruses (805). Users may access CoL China data via the website (http://www.sp2000.org.cn) or download data via an API (Application Program Interface). We developed a platform for species data collection and the on-line Taxonomic Tree Tool (TTT, http://ttt.biodinfo.org/) for data analysis, which integrates animal data with plant and microbial data into annual checklists and maintains the CoL China database system.

TTT is a web-based platform for managing and comparing taxonomic trees. It allows users to create their own taxonomic trees in four ways - manual input, uploading to XML (Extensible Markup Language), manually selecting taxa from template trees provided by

© Ji L. This is an open access article distributed under the terms of the Creative Commons Attribution License (CC BY 4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

TTT, or automatically selecting taxa from template trees according to a species list. Users can share their trees with registered users and compare them with the public trees. TTT provides a tool for comparing different trees to focus on the spots where more attention should be paid by taxonomists or informatics scientists. The comparison tool explores taxonomic relationships from two trees and classifies the differences into contrasting types of relationships. The tool helps find the differences between the taxonomic positions for taxon A and taxon B and highlights these explicitly. Furthermore, it calculates the similarity of branches from two compared trees to help taxonomists judge whether the taxon groups chosen are the same or if it is necessary to continue drilling down the taxonomic trees to explore more differences. TTT can extract common or different parts of two compared trees and the result can be exported for further tree integration research.

Keywords

species checklist, China, checklist tool

Presenting author

Liqiang Ji